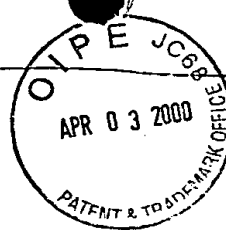SEQUENCE LISTING

<110> Sakowicz, Roman
       Goldstein, Lawrence S. B.
       The Regents of the University of California

<120> Identification and Expression of a Novel Kinesin Motor
       Protein

<130> 18557C-000710US

<140> US 09/235,416
<141> 1999-01-22

<150> WO PCT/US99/01355
<151> 1999-01-22

<150> US 60/072,361
<151> 1998-01-23

<160> 7

<170> PatentIn Ver. 2.0

<210> 1
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<212> PRT
<213> Thermomyces lanuginosus

<220>
<223> TL-gamma ATP-dependent plus end-directed
       microtubule motor protein

<220>
<221> DOMAIN
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<223> kinesin-like microtubule motor domain

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<221> DOMAIN
<222> (358)..(442)
<223> neck domain links motor domain to stalk domain

<220>
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<223> stalk domain, unc-104 family domain

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Gly Asn Gln Thr Ile Leu Thr Pro Pro Pro Gly Ala Glu Glu Lys Ala
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Arg Lys Ser Gly Lys Thr Ile Met Asp Gly Pro Lys Ala Phe Ala Phe
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Asp Arg Ser Tyr Trp Ser Phe Asp Lys Asn Ala Pro Asn Tyr Ala Arg
65              70              75                          80

Gln Glu Asp Leu Phe Gln Asp Leu Gly Val Pro Leu Leu Asp Asn Ala
            85              90                      95

Phe Lys Gly Tyr Asn Asn Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser
        100             105             110

Gly Lys Ser Tyr Ser Met Met Gly Tyr Gly Lys Glu His Gly Val Ile
        115             120             125

Pro Arg Ile Cys Gln Asp Met Phe Arg Arg Ile Asn Glu Leu Gln Lys
    130             135             140

Asp Lys Asn Leu Thr Cys Thr Val Glu Val Ser Tyr Leu Glu Ile Tyr
145             150             155                         160

Asn Glu Arg Val Arg Asp Leu Leu Asn Pro Ser Thr Lys Gly Asn Leu
            165             170             175

Lys Val Arg Glu His Pro Ser Thr Gly Pro Tyr Val Glu Asp Leu Ala
        180             185             190

Lys Leu Val Val Arg Ser Phe Gln Glu Ile Glu Asn Leu Met Asp Glu
        195             200             205

Gly Asn Lys Ala Arg Thr Val Ala Ala Thr Asn Met Asn Glu Thr Ser
    210             215             220

Ser Arg Ser His Ala Val Phe Thr Leu Thr Leu Thr Gln Lys Trp His
225             230             235                         240

Asp Glu Glu Thr Lys Met Asp Thr Glu Lys Val Ala Lys Ile Ser Leu
            245             250             255

Val Asp Leu Ala Gly Ser Glu Arg Ala Thr Ser Thr Gly Ala Thr Gly
            260             265             270

Ala Arg Leu Lys Glu Gly Ala Glu Ile Asn Arg Ser Leu Ser Thr Leu
        275             280             285

Gly Arg Val Ile Ala Ala Leu Ala Asp Met Ser Ser Gly Lys Gln Lys
    290             295             300

Lys Asn Gln Leu Val Pro Tyr Arg Asp Ser Val Leu Thr Trp Leu Leu
·305            310             315                         320

Lys Asp Ser Leu Gly Gly Asn Ser Met Thr Ala Met Ile Ala Ala Ile
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Ser Pro Ala Asp Ile Asn Phe Glu Glu Thr Leu Ser Thr Leu Arg Tyr
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Ala Asp Ser Ala Lys Arg Ile Lys Asn His Ala Val Val Asn Glu Asp
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Pro Asn Ala Arg Met Ile Arg Glu Leu Lys Glu Glu Leu Ala Gln Leu
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Arg Ser Lys Leu Gln Ser Ser Gly Gly Gly Gly Gly Gly Ala Gly Gly
385             390             395                 400

Ser Gly Gly Pro Val Glu Glu Ser Tyr Pro Pro Asp Thr Pro Leu Glu
            405             410             415

Lys Gln Ile Val Ser Ile Gln Gln Pro Asp Ala Thr Val Lys Lys Met
            420             425             430

Ser Lys Ala Glu Ile Val Glu Gln Leu Asn Gln Ser Glu Lys Leu Tyr
    435             440             445

Arg Asp Leu Asn Gln Thr Trp Glu Glu Lys Leu Ala Lys Thr Glu Glu
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Ile His Lys Glu Arg Glu Ala Ala Leu Glu Glu Leu Gly Ile Ser Ile
465             470             475                 480

Glu Lys Gly Phe Val Gly Pro Tyr His Ser Lys Glu Met Pro His Leu
            485             490             495

Val Asn Leu Ser Asp Asp Pro Leu Leu Ala Glu Cys Leu Val Tyr Asn
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Ile Lys Pro Gly Gln Thr Arg Val Gly Asn Val Asn Gln Asp Thr Gln
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Ala Glu Ile Arg Leu Asn Gly Ser Lys Ile Leu Lys Glu His Cys Thr
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Phe Glu Asn Val Asp Asn Val Val Thr Ile Val Pro Asn Glu Lys Ala
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Ala Val Met Val Asn Gly Val Arg Ile Asp Lys Pro Thr Arg Leu Arg
            565             570             575

Ser Gly Tyr Arg Ile Ile Leu Gly Asp Phe His Ile Phe Arg Phe Asn
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His Pro Glu Glu Ala Arg Ala Glu Arg Gln Glu Gln Ser Leu Leu Arg
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His Ser Val Thr Asn Ser Gln Leu Gly Ser Pro Ala Pro Gly Arg His
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Asp Arg Thr Leu Ser Lys Ala Gly Ser Asp Ala Asp Gly Asp Ser Arg
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Ser Asp Ser Pro Leu Pro His Phe Arg Gly Lys Asp Ser Asp Trp Phe
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Tyr Ala Arg Arg Glu Ala Ala Ser Ala Ile Leu Gly Leu Asp Gln Lys
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Ile Ser His Leu Thr Asp Asp Glu Leu Asp Ala Leu Phe Asp Asp Val
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Gln Lys Ala Arg Ala Val Arg Arg Gly Leu Val Glu Asp Asn Glu Asp
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Ser Asp Ser Gln Ser Ser Phe Pro Val Arg Asp Lys Tyr Met Ser Asn
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Gly Thr Ile Asp Asn Phe Ser Leu Asp Thr Ala Ile Thr Met Pro Gly
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Thr Pro Arg Ser Asp Asp Asp Gly Asp Ala Leu Phe Phe Gly Asp Lys
            740   745   750

Lys Ser Lys Gln Asp Ala Ser Asn Val Asp Val Glu Glu Leu Arg Gln
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Gln Gln Ala Gln Met Glu Glu Ala Leu Lys Thr Ala Lys Gln Glu Phe
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<223> TL-gamma ATP-dependent plus end-directed
      microtubule motor protein

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cctccgggtg ccgaagagaa ggcgcgtaaa agtggcaaaa ctattatgga tggcccgaag 180
gcatttgcgt tcgatcggtc gtattggtcc tttgacaaga atgctcccaa ctatgcgaga 240
caggaagacc tattccaaga tctcggagtc ccgcttctgg ataatgcatt caagggttat 300
aacaattgta tcttcgccta cggtcagacc ggttcgggca agtcctattc aatgatgggc 360
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cacccgtcga ccggccccta cgtggaggac ttggcgaagc tggtcgtgcg atcattccaa 600
gaaatcgaaa atctcatgga tgagggcaac aaagccagaa cggttgccgc cacaaacatg 660
aacgagacat ccagtcgatc ccacgccgtc ttcactttga ccttgacgca aaagtggcat 720
gatgaagaga ccaaaatgga cacagagaag gttgcgaaga tcagtctggt agatttggcg 780
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aagaccgagg aaatccacaa ggaacgagaa gcggcgctcg aggagctggg tatcagcatc 1440
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

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<210> 4
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<210> 5
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:degenerate
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<223> n = a, c, g or t

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<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

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      reverse primer

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<223> n = a, c, g or t

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<400> 7
gcgcgaattc tcdctnccdg cvarrtcnac                                    30
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